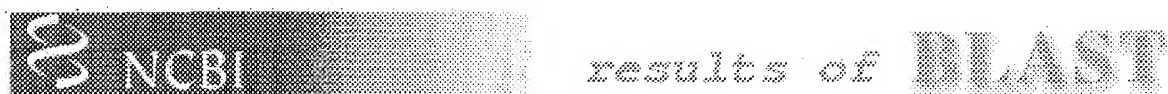


Sequences producing significant alignments:

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gi 33871813 gb BC009951.2 	Homo sapiens collectin sub-famil...	196	6e-48	
gi 40548419 ref NM_199235.1 	Homo sapiens collectin sub-fam...	196	6e-48	
gi 40548418 ref NM_024027.3 	Homo sapiens collectin sub-fam...	196	6e-48	
gi 15321567 gb AC010907.10 	Homo sapiens BAC clone RP11-568...	120	5e-25	
gi 31432982 gb AE017111.1 	Oryza sativa (japonica cultivar-...	41	0.63	
gi 20270142 gb AC068924.11 	Oryza sativa chromosome 10 BAC ...	41	0.63	
gi 24395000 emb AL732493.17 	Mouse DNA sequence from clone ...	41	0.63	
gi 34495171 gb AC140307.3 	Mus musculus BAC clone RP23-389D...	39	2.5	
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gi 29469606 gb AC105049.4 	Homo sapiens chromosome 8, clone...	39	2.5	
gi 37591141 dbj AP004111.2 	Oryza sativa (japonica cultivar...	39	2.5	
gi 12833583 dbj AK003121.1 	Mus musculus adult male heart c...	39	2.5	
gi 32980006 dbj AK069982.1 	Oryza sativa (japonica cultivar...	39	2.5	
gi 11876088 emb AL445586.6 	Human DNA sequence from clone R...	39	2.5	
gi 6562842 emb AJ010061.1 REU010061	Ralstonia eutropha inse...	39	2.5	
gi 18103850 emb AL137779.6 CNS01DWM	Human chromosome 14 DNA...	39	2.5	

gi 10947023 gb AC011510.7 AC011510	Homo sapiens chromosome ...	39	2.5	
gi 12330718 emb AL138720.19	Human DNA sequence from clone ...	39	2.5	
gi 40254386 ref NM_177049.4	Mus musculus RIKEN cDNA 933015...	37	10	
gi 22026879 ref NM_137185.2	Drosophila melanogaster CG8155...	37	10	
gi 22857857 gb AC125409.3	Mus musculus BAC clone RP23-1270...	37	10	
gi 30931355 gb BC052722.1	Mus musculus RIKEN cDNA 9330157P...	37	10	
gi 30354381 gb BC052049.1	Mus musculus RIKEN cDNA 9330157P...	37	10	
gi 30851498 gb BC052376.1	Mus musculus RIKEN cDNA 9330157P...	37	10	
gi 37537604 gb AC116038.3	Homo sapiens chromosome 3 clone ...	37	10	
gi 37059962 gb AC136986.6	Mus musculus chromosome 12, clon...	37	10	
gi 2979573 gb AC002331.1 HUAC002331	Homo sapiens Chromosome...	37	10	
gi 23343653 gb AC123511.3	Homo sapiens 3 BAC RP11-637F14 (...)	37	10	
gi 34535062 dbj AK127934.1	Homo sapiens cDNA FLJ46043 fis,...	37	10	
gi 29294017 gb AC008756.9	Homo sapiens chromosome 16 clone...	37	10	
gi 38198204 dbj AB099712.1	Mus musculus JP-4 mRNA for junc...	37	10	
gi 22417370 gb AC116035.2	Homo sapiens chromosome 3 clone ...	37	10	
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gi 21930249 gb AC104450.2	Homo sapiens chromosome 3 clone ...	37	10	
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gi 24643469 ref NM_078695.2	Drosophila melanogaster Rab-pr...	35	41	
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gi 22655817 gb AC129908.4	Homo sapiens chromosome 18, clon...	35	41	

**BLASTN 2.2.8 [Jan-05-2004]**Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

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(1170 letters)

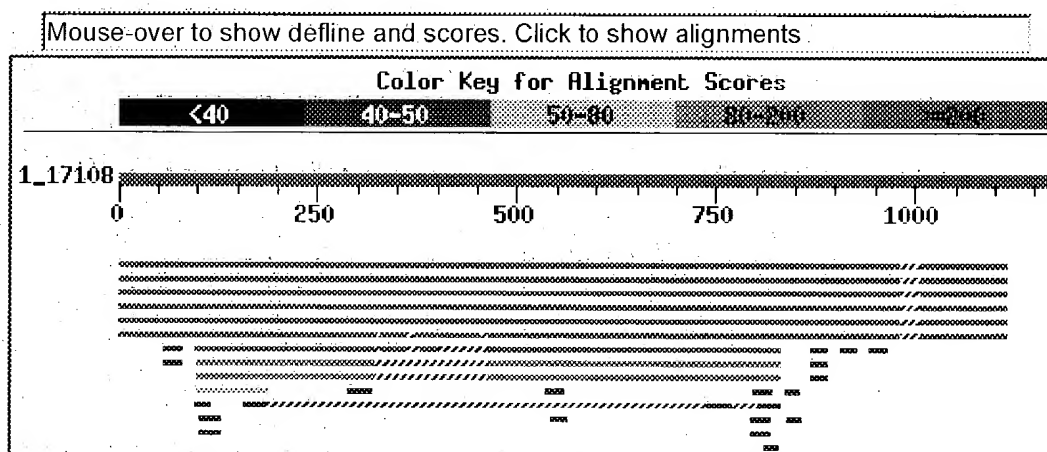
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2,102,977 sequences; 10,130,642,339 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 51 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Score E
(bits) Value

gi 32990875 gb BC000078.2	Homo sapiens collectin sub-famil...	1356	0.0	
gi 37182002 gb AY358439.1	Homo sapiens clone DNA59848 RGNL...	1356	0.0	
gi 40548418 ref NM_024027.3	Homo sapiens collectin sub-fam...	1356	0.0	
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gi 40548419 ref NM_199235.1	Homo sapiens collectin sub-fam...	963	0.0	
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gi 38049423 ref XM_283054.2	Mus musculus collectin sub-fam...	197	4e-47	
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gi 33417123 gb BC056052.1	Xenopus laevis collectin sub-fam...	47	0.070	
gi 14151043 gb AC011899.5	Homo sapiens BAC clone RP11-452C...	43	1.2	
gi 34148207 gb AY357890.1	Glomerella cingulata mating-type...	43	1.2	
gi 26190555 gb AC131971.9	Homo sapiens chromosome 11, clon...	43	1.2	
gi 1935053 gb AC001228.1	HSAC001228 244Kb Contig from Human...	43	1.2	
gi 11121080 emb AL391804.8	Human DNA sequence from clone R...	43	1.2	
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gi 20270142 gb AC068924.11	Oryza sativa chromosome 10 BAC ...	41	4.8	
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gi 341502 gb M26461.1	RICRG18S Rice 18S ribosomal RNA (18S ...	41	4.8	

2003 or 2004

Alignments

Get selected sequences

Select all

Deselect all

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

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Query: 773 tcgggcggtgmm-cgacgtggcctgccacaccaccatgtacttcatgtgtgagtttgac 831
|||||

Sbjct: 967 tcgggcggtggaacgacgtggcctgccacaccaccatgtacttcatgtgtgagtttgac 1026

Query: 832 m-ggagm-catgtg-gcctcaggctggggctgcccattgggggccccacatgtccctgca 888
|||||

Sbjct: 1027 aaggagaacatgtgagcctcaggctggggctgcccattgggggccccacatgtccctgca 1086

Query: 889 gggttggcagggacagagcccagaccatggtgccagccaggagctgtccctctgtg-mg 947
|||||

Sbjct: 1087 gggttggcagggacagagcccagaccatggtgccagccaggagctgtccctctgtgaag 1146

Query: 948 ggtggaggctcactgagtagagggtgtgtct 980
|||||

Sbjct: 1147 ggtggaggctcactgagtagagggtgtgtct 1179

Score = 394 bits (194), Expect = e-106
Identities = 253/268 (94%), Gaps = 9/268 (3%)
Strand = Plus / Plus

Query: 1 gcgacgggcaggagcggcgcttcgcctagcgcggtgctcaggagttggtgtcctgcctgcg 60
|||||

Sbjct: 81 gcgacgggcaggagcggcgcttcgcctagcgcggtgctcaggagttggtgtcctgcctgcg 140

Query: 61 ctacagg-tgaggggg-mtctggccctggtggcgcttct-mtcagcctggccttctgtca 117
|||||

Sbjct: 141 ctacaggatgagggggaatctggccctggtggcgcttctaatcagcctggccttctgtca 200

Query: 118 ctgctgccatctggacatcctcagccggtggcgatgacgcctgctctgtgcagatcctc 177
|||||

Sbjct: 201 ctgctgccatctggacatcctcagccggtggcgatgacgcctgctctgtgcagatcctc 260

Query: 178 gtccctggcctc--wggggatgcgggagag-mgggagac--wggcgccccggacggcct 232
|||||

Sbjct: 261 gtccctggcctcaaaggggatgcgggagagaaggagacaaaggcgccccggacggcct 320

Query: 233 gg-mgagtcggcccccacgggagaaaaag 259
||

Sbjct: 321 ggaagagtcggcccccacgggagaaaaag 348

Score = 132 bits (65), Expect = 1e-27
Identities = 105/117 (89%), Gaps = 6/117 (5%)
Strand = Plus / Plus

Query: 1007 gtgttcctgggggtgctgtctctgm--gmgcagagtttcattacctgtattgtagcccca 1064
|||||
Sbjct: 1219 gtgttcctgggggtgctgtctctgaagaagcagagtttcattacctgtattgtagcccca 1278

Query: 1065 tgtcattatgt-mttattaccag-mttgctcttccat--wgcttgtgcctttgtcc 1117
|||||
Sbjct: 1279 tgtcattatgtattattaccagaattgctcttccataaagcttgtgcctttgtcc 1335

>gi|40548419|ref|NM_199235.1| Homo sapiens collectin sub-family member 11 (COL
variant 2, mRNA
Length = 1399

Score = 963 bits (474), Expect = 0.0
Identities = 693/753 (92%); Gaps = 31/753 (4%)
Strand = Plus / Plus

Query: 259 ggagacatgggggacw--ggacagw--ggcagtgtgggtcgatggaaaaattgggtccc 314
|||||
Sbjct: 429 ggagacatgggggacaaaggacagaaaggcagtgtgggtcgatggaaaaattgggtccc 488

Query: 315 attggctctw--ggtgagg--ggagattccggtgacataggacccctgggtcctm-tgga 369
|||||
Sbjct: 489 attggctctaaagggtgagaaaggagattccggtgacataggacccctgggtcctaattgga 548

Query: 370 gm-ccaggcctcccatgtgagtgacgccagctgcgcm-ggccatcggggagatggacm-c 426
|
Sbjct: 549 gaaccaggcctcccatgtgagtgacgccagctgcgcaaggccatcggggagatggacaac 608

Query: 427 cagggtctctcagctgaccagcgagctcm-gttcatcmg--mtgctgtcgccggtgtgcgc 483
|||||
Sbjct: 609 cagggtctctcagctgaccagcgagctcaagttcatcaagaatgctgtcgccggtgtgcgc 668

Query: 484 gagacggagagc-mgatctacctgctggtg-mggaggag-mgcgctacgcggacgcccag 540
|||||
Sbjct: 669 gagacggagagcaagatctacctgctggtgaaggaggagaagcgctacgcggacgcccag 728

Query: 541 ctgtcctgccagggccgcgggggcacgctgagcatgccc-mggacgaggctgccaatggc 599
|||||
Sbjct: 729 ctgtcctgccagggccgcgggggcacgctgagcatgcccgaaggacgaggctgccaatggc 788

Query: 600 ctgatggccgcatacctggcgc-mgccggcctggcccgtgttctcatcggcac-mcgac 657
|||||
Sbjct: 789 ctgatggccgcatacctggcgcgaagccggcctggcccgtgttctcatcggcacacacgac 848

Query: 658 ctggag-mggagggcgcccttcgtgtactctgaccactcccccatgcgaccttc--mcmg 714
|||||
Sbjct: 849 ctggagaaggaggcgcccttcgtgtactctgaccactcccccatgcgaccttcaacaag 908